

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/971,172DATE: 06/26/98
TIME: 13:36:11

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This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4 (i) APPLICANT: Goodman, Corey S.
5 Kidd, Thomas
6 Mitchell, Kevin
7 Tear, Guy
8 (ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and
9 Nucleic Acids
10 (iii) NUMBER OF SEQUENCES: 12
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
13 (B) STREET: 75 DENISE DRIVE
14 (C) CITY: HILLSBOROUGH
15 (D) STATE: CALIFORNIA
16 (E) COUNTRY: USA
17 (F) ZIP: 94010
18 (v) COMPUTER READABLE FORM:
19 (A) MEDIUM TYPE: Floppy disk
20 (B) COMPUTER: IBM PC compatible
21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
23 (vi) CURRENT APPLICATION DATA:
24 (A) APPLICATION NUMBER:
25 (B) FILING DATE:
26 (C) CLASSIFICATION:
27 (viii) ATTORNEY/AGENT INFORMATION:
28 (A) NAME: OSMAN, RICHARD A
29 (B) REGISTRATION NUMBER: 36,627
30 (C) REFERENCE/DOCKET NUMBER: B98-006
31 (ix) TELECOMMUNICATION INFORMATION:
32 (A) TELEPHONE: (650) 343-4341
33 (B) TELEFAX: (650) 343-4342
34
35 (2) INFORMATION FOR SEQ ID NO:1:
36 (i) SEQUENCE CHARACTERISTICS:
37 (A) LENGTH: 4188 base pairs
38 (B) TYPE: nucleic acid
39 (C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear
41 (ii) MOLECULE TYPE: cDNA
42 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
43 ATGCATCCCA TGCATCCCGA AAACCACGCC ATCGCCCGGA GCACGAGCAC CACTAATAAC 60
44 CCATCTCGCA GTCGGAGCAG CAGGATGTGG CTCTGCCCCG CCTGGCTGCT CCTCGTCCTG 120
45 GTGGCCAGCA ATGGCCTGCC AGCAGTCAGA GGCCAGTACC AATCGCCACG TATCATCGAG 180
46 CATCCACGG ATCTGGTCGT TAAGAAGAAT GAACCCGCCA CGCTCAACTG CAAAGTGGAG 240

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49	GGCAAGAAGG	AGCAGGACGG	CGGAGAGTAC	TGGTGCGTGG	CCAAGAACCG	AGTGGGCCAG	420
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51	CCCAAAGACA	CGCGAGTGGC	CAAAGGCGAG	ACGGCTCTGC	TGGAGTGTGG	GCCGCCCCAA	540
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63	GATGGAATC	TGCAGATTAC	GGATGTGCGG	CAGGAAGACG	AAGGCTACTA	TGTGTGTTCC	1260
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71	AGTCGCACCA	GCATTAGTCT	TCGTTGGGCT	AAAAGCCAAG	AGAAACCCGG	AGCTGTGGGC	1740
72	CCAATCATTG	GATACACTGT	AGAGTACTTC	AGTCCGGATC	TGCAAACTGG	TTGGATTGTG	1800
73	GCTGCCCATC	GAGTCGGCGA	CACTCAAGTC	ACTATCTCGG	GTCTCACTCC	TGGCACTTCG	1860
74	TATGTGTTCC	TAGTTAGAGC	TGAGAAATAC	CAGGGTATTT	CTGTGCCTTC	CGGCTTATCA	1920
75	AATGTTATTA	AAACCATTTGA	GGCAGATTTT	GATGCAGCTT	CTGCCAATGA	TTTGTACAGCA	1980
76	GCTCGAACTT	TGCTGACAGG	AAAGTCGGTG	GAGCTAATAG	ATGCCTCGGC	TATCAATGCT	2040
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78	TGCGCATAC	ACTATAAGGA	TGCCAGTGTA	CCATCCGCAC	AGTATCACTC	GATCACTGTT	2160
79	ATGGATGCCCT	CTGCAGAAATC	GTTTGTGGTG	GGAAACCTTA	AGAAGTACAC	CAAGTATGAG	2220
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82	CAACAGCCG	GTTGGGTGCG	TTGGACTCCG	CCACCCTCCC	AGCACCACAA	TGGCAATTTG	2400
83	TATGGCTACA	AGATTGAGGT	CAGCGCCGGT	AACACCATGA	AGGTGCTGGC	CAATATGACT	2460
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86	TTCATGGACC	CCACCCATCA	TGTGCATCCG	CCACGGGCAC	ATCCAAGCGG	CACCCATGAT	2640
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102 TCGGCAGTGG CTGGCGGCAC CCAGAACCGC TATCAGATAA CGCCCACAAA CCAACATCCG 3600
103 CCACAGTTAC CGGCCTACTT TGCCACCACG GGTCCAGGAG GAGCTGTACC ACCCAACCAC 3660
104 CTGCCATTTG CCACACAGCG TCATGCAGCC AGCGAGTACC AGGCTGGACT GAATGCAGCG 3720
105 CGATGTGCCC AAAGCCGCGC CTGCAACAGC TGCATGCCTT TGGCCACACC CTCGCCCATG 3780
106 CAACCCCCAC CGCCAGTTCC CGTACCCGAG GGCTGGTACC AACCAGTGCA TCCCAATAGC 3840
107 CACCCGATGC ACCCGACCTC CTCCAACCAC CAGATCTACC AGTGCTCCTC CGAGTGCTCG 3900
108 GATCACTCGA GGAGCTCGCA GAGTCACAAG CGGCAGCTGC AGCTCGAGGA GCACGGCAGC 3960
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111 TGCAATAGCT CCCGCGAGGG CGACACCTGC TCCTGCAGCG AGGGATCCTG TCTTTACGCC 4140
112 GAGGCGGGCG AGCCGGCGCC TCGTCAAATG ACTGCTAAGA ACACCTAA 4188

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113

114 (2) INFORMATION FOR SEQ ID NO:2:

115 (i) SEQUENCE CHARACTERISTICS:

116 (A) LENGTH: 1395 amino acids

117 (B) TYPE: amino acid

118 (C) STRANDEDNESS: single

119 (D) TOPOLOGY: linear

120 (ii) MOLECULE TYPE: peptide

121 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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125 20 25 30
126 Pro Ala Trp Leu Leu Leu Val Leu Val Ala Ser Asn Gly Leu Pro Ala
127 35 40 45
128 Val Arg Gly Gln Tyr Gln Ser Pro Arg Ile Ile Glu His Pro Thr Asp
129 50 55 60
130 Leu Val Val Lys Lys Asn Glu Pro Ala Thr Leu Asn Cys Lys Val Glu
131 65 70 75 80
132 Gly Lys Pro Glu Pro Thr Ile Glu Trp Phe Lys Asp Gly Glu Pro Val
133 85 90 95
134 Ser Thr Asn Glu Lys Lys Ser His Arg Val Gln Phe Lys Asp Gly Ala
135 100 105 110
136 Leu Phe Phe Tyr Arg Thr Met Gln Gly Lys Lys Glu Gln Asp Gly Gly
137 115 120 125
138 Glu Tyr Trp Cys Val Ala Lys Asn Arg Val Gly Gln Ala Val Ser Arg
139 130 135 140
140 His Ala Ser Leu Gln Ile Ala Val Leu Arg Asp Asp Phe Arg Val Glu
141 145 150 155 160
142 Pro Lys Asp Thr Arg Val Ala Lys Gly Glu Thr Ala Leu Leu Glu Cys
143 165 170 175
144 Gly Pro Pro Lys Gly Ile Pro Glu Pro Thr Leu Ile Trp Ile Lys Asp
145 180 185 190
146 Gly Val Pro Leu Asp Asp Leu Lys Ala Met Ser Phe Gly Ala Ser Ser
147 195 200 205
148 Arg Val Arg Ile Val Asp Gly Gly Asn Leu Leu Ile Ser Asn Val Glu
149 210 215 220
150 Pro Ile Asp Glu Gly Asn Tyr Lys Cys Ile Ala Gln Asn Leu Val Gly
151 225 230 235 240
152 Thr Arg Glu Ser Ser Tyr Ala Lys Leu Ile Val Gln Val Lys Pro Tyr

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159		290					295				300					
160	Asp	Glu	Lys	Ser	Leu	Glu	Ile	Ser	Asn	Ile	Thr	Pro	Thr	Asp	Glu	Gly
161	305					310					315				320	
162	Thr	Tyr	Val	Cys	Glu	Ala	His	Asn	Asn	Val	Gly	Gln	Ile	Ser	Ala	Arg
163				325						330					335	
164	Ala	Ser	Leu	Ile	Val	His	Ala	Pro	Pro	Asn	Phe	Thr	Lys	Arg	Pro	Ser
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168	Ser	Gly	Asn	Pro	Pro	Pro	Ser	Val	Phe	Trp	Thr	Lys	Glu	Gly	Val	Ser
169		370					375					380				
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174	Tyr	Val	Cys	Ser	Ala	Phe	Ser	Val	Val	Asp	Ser	Ser	Thr	Val	Arg	Val
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182	Asp	Gly	His	Ala	Val	Gln	Ala	Gly	Asn	Arg	Tyr	Ser	Ile	Ile	Gln	Gly
183				485						490				495		
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185			500						505				510			
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191	545					550					555				560	
192	Ser	Arg	Thr	Ser	Ile	Ser	Leu	Arg	Trp	Ala	Lys	Ser	Gln	Glu	Lys	Pro
193				565						570					575	
194	Gly	Ala	Val	Gly	Pro	Ile	Ile	Gly	Tyr	Thr	Val	Glu	Tyr	Phe	Ser	Pro
195			580						585				590			
196	Asp	Leu	Gln	Thr	Gly	Trp	Ile	Val	Ala	Ala	His	Arg	Val	Gly	Asp	Thr
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198	Gln	Val	Thr	Ile	Ser	Gly	Leu	Thr	Pro	Gly	Thr	Ser	Tyr	Val	Phe	Leu
199		610					615					620				
200	Val	Arg	Ala	Glu	Asn	Thr	Gln	Gly	Ile	Ser	Val	Pro	Ser	Gly	Leu	Ser
201	625					630					635				640	
202	Asn	Val	Ile	Lys	Thr	Ile	Glu	Ala	Asp	Phe	Asp	Ala	Ala	Ser	Ala	Asn
203				645						650					655	
204	Asp	Leu	Ser	Ala	Ala	Arg	Thr	Leu	Leu	Thr	Gly	Lys	Ser	Val	Glu	Leu
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208	Leu	His	Val	Ser	Ala	Asp	Glu	Lys	Tyr	Val	Glu	Gly	Leu	Arg	Ile	His
209			690					695					700			
210	Tyr	Lys	Asp	Ala	Ser	Val	Pro	Ser	Ala	Gln	Tyr	His	Ser	Ile	Thr	Val
211			705					710					715			720
212	Met	Asp	Ala	Ser	Ala	Glu	Ser	Phe	Val	Val	Gly	Asn	Leu	Lys	Lys	Tyr
213					725					730					735	
214	Thr	Lys	Tyr	Glu	Phe	Phe	Leu	Thr	Pro	Phe	Phe	Glu	Thr	Ile	Glu	Gly
215				740					745					750		
216	Gln	Pro	Ser	Asn	Ser	Lys	Thr	Ala	Leu	Thr	Tyr	Glu	Asp	Val	Pro	Ser
217				755					760					765		
218	Ala	Pro	Pro	Asp	Asn	Ile	Gln	Ile	Gly	Met	Tyr	Asn	Gln	Thr	Ala	Gly
219			770					775					780			
220	Trp	Val	Arg	Trp	Thr	Pro	Pro	Pro	Ser	Gln	His	His	Asn	Gly	Asn	Leu
221			785					790					795			800
222	Tyr	Gly	Tyr	Lys	Ile	Glu	Val	Ser	Ala	Gly	Asn	Thr	Met	Lys	Val	Leu
223					805					810					815	
224	Ala	Asn	Met	Thr	Leu	Asn	Ala	Thr	Thr	Thr	Ser	Val	Leu	Leu	Asn	Asn
225				820						825				830		
226	Leu	Thr	Thr	Gly	Ala	Val	Tyr	Ser	Val	Arg	Leu	Asn	Ser	Phe	Thr	Lys
227				835					840					845		
228	Ala	Gly	Asp	Gly	Pro	Tyr	Ser	Lys	Pro	Ile	Ser	Leu	Phe	Met	Asp	Pro
229			850					855					860			
230	Thr	His	His	Val	His	Pro	Pro	Arg	Ala	His	Pro	Ser	Gly	Thr	His	Asp
231			865					870					875			880
232	Gly	Arg	His	Glu	Gly	Gln	Asp	Leu	Thr	Tyr	His	Asn	Asn	Gly	Asn	Ile
233					885					890					895	
234	Pro	Pro	Gly	Asp	Ile	Asn	Pro	Thr	Thr	His	Lys	Lys	Thr	Thr	Asp	Tyr
235				900					905					910		
236	Leu	Ser	Gly	Pro	Trp	Leu	Met	Val	Leu	Val	Cys	Ile	Val	Leu	Leu	Val
237				915					920					925		
238	Leu	Val	Ile	Ser	Ala	Ala	Ile	Ser	Met	Val	Tyr	Phe	Lys	Arg	Lys	His
239			930					935					940			
240	Gln	Met	Thr	Lys	Glu	Leu	Gly	His	Leu	Ser	Val	Val	Ser	Asp	Asn	Glu
241						950						955				960
242	Ile	Thr	Ala	Leu	Asn	Ile	Asn	Ser	Lys	Glu	Ser	Leu	Trp	Ile	Asp	His
243					965						970				975	
244	His	Arg	Gly	Trp	Arg	Thr	Ala	Asp	Thr	Asp	Lys	Asp	Ser	Gly	Leu	Ser
245				980					985					990		
246	Glu	Ser	Lys	Leu	Leu	Ser	His	Val	Asn	Ser	Ser	Gln	Ser	Asn	Tyr	Asn
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248	Asn	Ser	Asp	Gly	Gly	Thr	Asp	Tyr	Ala	Glu	Val	Asp	Thr	Arg	Asn	Leu
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251			1025					1030				1035				1040
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256	Ser	Asp	Ala	Phe	Ala	Gly	Gln	Val	Pro	Ala	Val	Pro	Val	Val	Lys	Ser
257				1075					1080					1085		
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